RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/601,371

DATE: 10/01/2001
TIME: 09:42:35

Input Set : A:\49927-sequence.txt
Output Set: N:\CRF3\10012001\I601371.raw

```
  4 <110> APPLICANT: SEYA, Tsukasa                                ENTERED
  5          MATSUMOTO, Misako
  7 <120> TITLE OF INVENTION: CYTOKINE INDUCERS COMPRISING M161AG
 10 <130> FILE REFERENCE: 49927 (71526)
 12 <140> CURRENT APPLICATION NUMBER: 09/601,371
 13 <141> CURRENT FILING DATE: 2000-12-05
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP99/00414              ENTERED
 16 <151> PRIOR FILING DATE: 1999-02-01
 18 <150> PRIOR APPLICATION NUMBER: 10-32384/1998
 19 <151> PRIOR FILING DATE: 1998-01-30
 21 <160> NUMBER OF SEQ ID NOS: 2
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1621
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Mycoplasma Fermentas
 30 <400> SEQUENCE: 1
 31  aaggagatta tatgaaaaag tcaaaaaaaa ttttattagg attgagtcct attgctgcta     60
 32  ttcttcctgc agtagctgtt tcttgtggaa acaacgatga atccaatatt tcattcaaag    120
 33  agaaagatat tagtaaatat accacaacaa atgctaatgg aaaacaagtt gttaaaaacg    180
 34  ctgaattgtt aaaattgaaa ccagttctta ttacagatga aggtaaaatt gatgataaat    240
 35  catttaacca atcagctttt gaagctttaa aagctataaa taaacaaact ggtattgaaa    300
 36  ttaacaatgt tgaacctagc tcaaactttg aaagtgctta caacagtgca ctttcagccg    360
 37  gacacaaaat ttgagtactt aatggcttca aacaccaaca atctattaaa caatacattg    420
 38  atgctcacag agaagaactt gaaagaaatc aaatcaaaat cattggtatc gactttgata    480
 39  ttgaaacaga gtacaagtga ttctactcat tacaattcaa tattaaagaa tctgcattta    540
 40  caacaggcta tgcaattgca agttgattaa gtgaacaaga tgaaagtaaa agagttgttg    600
 41  catcatttgg tggaggtgca ttcccaggtg ttacaacatt taacgaaggt tttgcaaaag    660
 42  gtattctata ctacaaccaa aaacataaat caagtaaaat ttaccacaca tcacctgtta    720
 43  aattagactc aggttttact gctggtgaaa aaatgaacac tgttattaat aatgtttat     780
 44  cttcaacacc agctgatgtt aaatacaacc cacatgttat cttatctgtt gctggacctg    840
 45  ctacatttga aactgtaaga ttagcaaaca aaggtcaata tgtaattggt gttgactcag    900
 46  accaaggcat gattcaagac aaagacagaa ttcttacatc agttctaaaa cacattaaac    960
 47  aagctgttta tgaaacatta ttagatctta ttcttgaaaa agaagaagga tataaaccat   1020
 48  atgtagttaa agacaaaaaa gcagacaaaa aatgaagcca ctttggaact caaaaagaaa   1080
 49  aatgaatcgg tgtcgcagaa aaccacttct caaatacaga agaacaagca aaaattaata   1140
 50  acaaaattaa agaagcaatt aaaatgttta agaattacc agaagatttc gttaaatata    1200
 51  ttaatagtga caaagcttta aaagatggta ataaaattga caatgttagt gaaagattag   1260
 52  aagcaattat ttctgctatt aacaaggcag caaaataatt aatcaaaaaa atgctggaaa   1320
 53  atatccagca ttttttattt taaatatgaa aaaagtatat ttttttgtta atttttgaag   1380
 54  aaaattagata aaacagtttt tccgtttttg tcttcaaata agataaataa gagaaaaaag   1440
 55  gttgtaaaac tgcctaagaa aaaaagagtt ggaaaacata aaagttaaag accaaattat   1500
 56  ttaactattt atgactttga gatggatacg gttcatgggt gtagaatgga tgaatatttc   1560
 57  attttgattt taataaatag attgactaga gaagtacact ttaaaaaaaa aaaaaaaaa    1620
 58  a                                                                   1621
 60 <210> SEQ ID NO: 2
 61 <211> LENGTH: 428
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62 <212> TYPE: PRT
63 <213> ORGANISM: Mycoplasma Fermentas
65 <400> SEQUENCE: 2
66  Met Lys Lys Ser Lys Lys Ile Leu Leu Gly Leu Ser Pro Ile Ala Ala
67   1               5                  10                  15
68  Ile Leu Pro Ala Val Ala Val Ser Cys Gly Asn Asn Asp Glu Ser Asn
69              20                  25                  30
70  Ile Ser Phe Lys Glu Lys Asp Ile Ser Lys Tyr Thr Thr Thr Asn Ala
71          35                  40                  45
72  Asn Gly Lys Gln Val Val Lys Asn Ala Glu Leu Leu Lys Leu Lys Pro
73      50                  55                  60
74  Val Leu Ile Thr Asp Glu Gly Lys Ile Asp Asp Lys Ser Phe Asn Gln
75  65                  70                  75                  80
76  Ser Ala Phe Glu Ala Leu Lys Ala Ile Asn Lys Gln Thr Gly Ile Glu
77                  85                  90                  95
78  Ile Asn Asn Val Glu Pro Ser Ser Asn Phe Glu Ser Ala Tyr Asn Ser
79                  100                 105                 110
80  Ala Leu Ser Ala Gly His Lys Ile Trp Val Leu Asn Gly Phe Lys His
81              115                 120                 125
82  Gln Gln Ser Ile Lys Gln Tyr Ile Asp Ala His Arg Glu Glu Leu Glu
83          130                 135                 140
84  Arg Asn Gln Ile Lys Ile Ile Gly Ile Asp Phe Asp Ile Glu Thr Glu
85  145                 150                 155                 160
86  Tyr Lys Trp Phe Tyr Ser Leu Gln Phe Asn Ile Lys Glu Ser Ala Phe
87                  165                 170                 175
88  Thr Thr Gly Tyr Ala Ile Ala Ser Trp Leu Ser Glu Gln Asp Glu Ser
89              180                 185                 190
90  Lys Arg Val Val Ala Ser Phe Gly Gly Gly Ala Phe Pro Gly Val Thr
91          195                 200                 205
92  Thr Phe Asn Glu Gly Phe Ala Lys Gly Ile Leu Tyr Tyr Asn Gln Lys
93          210                 215                 220
94  His Lys Ser Ser Lys Ile Tyr His Thr Ser Pro Val Lys Leu Asp Ser
95  225                 230                 235                 240
96  Gly Phe Thr Ala Gly Glu Lys Met Asn Thr Val Ile Asn Asn Val Leu
97                  245                 250                 255
98  Ser Ser Thr Pro Ala Asp Val Lys Tyr Asn Pro His Val Ile Leu Ser
99                  260                 265                 270
100 Val Ala Gly Pro Ala Thr Phe Glu Thr Val Arg Leu Ala Asn Lys Gly
101             275                 280                 285
102 Gln Tyr Val Ile Gly Val Asp Ser Asp Gln Gly Met Ile Gln Asp Lys
103         290                 295                 300
104 Asp Arg Ile Leu Thr Ser Val Leu Lys His Ile Lys Gln Ala Val Tyr
105 305                 310                 315                 320
106 Glu Thr Leu Leu Asp Leu Ile Leu Glu Lys Glu Glu Gly Tyr Lys Pro
107                 325                 330                 335
108 Tyr Val Val Lys Asp Lys Lys Ala Asp Lys Lys Trp Ser His Phe Gly
109             340                 345                 350
110 Thr Gln Lys Glu Lys Trp Ile Gly Val Ala Glu Asn His Phe Ser Asn
111             355                 360                 365
```

file://C:\Crf3\Outhold\VsrI601371.htm

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```
112   Thr Glu Glu Gln Ala Lys Ile Asn Asn Lys Ile Lys Glu Ala Ile Lys
113       370             375             380
114   Met Phe Lys Glu Leu Pro Glu Asp Phe Val Lys Tyr Ile Asn Ser Asp
115   385             390             395             400
116   Lys Ala Leu Lys Asp Gly Asn Lys Ile Asp Asn Val Ser Glu Arg Leu
117               405             410             415
118   Glu Ala Ile Ile Ser Ala Ile Asn Lys Ala Ala Lys
119           420             425
```

VERIFICATION SUMMARY
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